

## SEQUENCE LISTING

<110> ZOOROB, RIMA  
AUFFRAY, CHARLES  
CHAUSSE, ANNE-MARIE

<120> REAGENTS AND METHODS FOR DETECTING GENES RELATED TO  
MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH  
AS CHICKEN

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<141> 2000-07-24

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<150> FR 97/14669  
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<213> Gallus sp.

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 <211> 716  
 <212> DNA  
 <213> Gallus sp.

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 <213> Gallus sp.

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<210> 36  
 <211> 421  
 <212> DNA  
 <213> Gallus sp.

<220>  
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<223> "n" represents a, t, c, g, other or unknown

<400> 36

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<210> 37

<211> 684  
 <212> DNA  
 <213> Gallus sp.

<400> 37

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<210> 38

<211> 1920  
 <212> DNA  
 <213> Gallus sp.

<400> 38

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<210> 39  
 <211> 628  
 <212> DNA  
 <213> Gallus sp.

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<210> 40  
 <211> 372  
 <212> DNA  
 <213> Gallus sp.

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<210> 41  
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 <212> DNA  
 <213> Gallus sp.

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 <212> DNA  
 <213> Gallus sp.

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 <213> Gallus sp.

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 tcgcccacga aattgaacat gtgaatgc ttatctgcaat tggaaaaggcg cgcttccagt 180  
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 <211> 4846  
 <212> DNA  
 <213> Gallus sp.

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GALLUS SP. DNA

tgcacagg tgggcagga attggcacct gttggctct gggttgcag cagtagaaaa 1920  
 tgtaaacgtg gcctgcgtg gggatctgt tttccctgg caatggAAC agctttgggg 1980  
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<210> 45  
 <211> 546  
 <212> PRT  
 <213> Gallus sp.

<220>  
 <221> MOD\_RES  
 <222> (530)  
 <223> "Xaa" represents any, other or unknown amino acid

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 20 25 30  
 Leu Ser Ser Ala Val Thr Glu Leu Val Cys Asp Val Thr Phe Val Gly  
 35 40 45  
 Thr Leu Ser Arg Thr Gln Ser Arg Leu Gln Arg Arg Val Phe Ala Ala  
 50 55 60  
 Val Leu Arg Gln Ser Ile Thr Glu Leu Arg Ala Asp Gly Ala Gly Asp  
 65 70 75 80  
 Val Ala Met Arg Val Thr Arg Asp Ala Glu Asp Val Arg Glu Ala Leu  
 85 90 95  
 Gly Lys Ala Leu Ser Leu Leu Leu Trp Tyr Leu Ala Arg Gly Leu Cys  
 100 105 110  
 Leu Phe Ala Thr Met Ala Trp Leu Ser Pro Arg Met Ala Leu Leu Thr  
 115 120 125  
 Ala Leu Ala Leu Pro Leu Leu Ala Leu Pro Arg Ala Val Gly His  
 130 135 140  
 Phe Arg Gln Ala Leu Ala Pro Gln Met Gln Lys Ala Gln Ala Arg Ala  
 145 150 155 160  
 Ser Glu Val Ala Val Glu Thr Phe Gln Ala Met Ala Thr Val Arg Ser  
 165 170 175  
 Phe Ala Asn Glu Asp Gly Ala Ala His Tyr Arg Gln Arg Leu Gln  
 180 185 190  
 Gln Ser His Arg Leu Glu Lys Lys Asp Val Ala Leu Tyr Thr Ala Ser  
 195 200 205  
 Leu Trp Thr Ser Gly Phe Ser Ala Leu Ala Leu Lys Met Gly Ile Leu  
 210 215 220  
 Tyr Tyr Gly Gly Gln Leu Val Ala Ala Gly Thr Val Ser Thr Gly Asp  
 225 230 235 240  
 Leu Val Thr Phe Leu Leu Tyr Gln Ile Gln Phe Thr Asp Val Leu Glu  
 245 250 255  
 Val Leu Leu Asp Tyr Phe Pro Thr Leu Met Lys Ala Val Gly Ser Ser  
 260 265 270

Glu Lys Ile Phe Glu Phe Leu Asp Arg Glu Pro Gln Val Ser Pro Ser  
 275 280 285  
 Gly Thr Met Ala Pro Ala Asp Leu Gln Gly His Leu Gln Leu Glu Asp  
 290 295 300  
 Val Trp Phe Ser Tyr Pro Gly Arg Gln Glu Thr Arg Pro Gln Gly Val  
 305 310 315 320  
 Ser Leu Glu Leu Arg Pro Gly Glu Val Leu Ala Leu Leu Gly Pro Pro  
 325 330 335  
 Gly Ala Gly Lys Ser Thr Leu Val Ala Leu Val Ser Arg Leu His Gln  
 340 345 350  
 Pro Thr Ala Gly Arg Leu Leu Leu Asp Gly His Pro Leu Pro Ala Tyr  
 355 360 365  
 Gln His Ser Tyr Leu Cys Arg Gln Val Ala Val Val Pro Gln Glu Pro  
 370 375 380  
 Leu Leu Phe Ala Arg Ser Leu His Ala Asn Ile Ser Tyr Gly Leu Gly  
 385 390 395 400  
 Gly Cys Ser Arg Ala Gln Val Thr Ala Ala Ala Arg Arg Val Gly Ala  
 405 410 415  
 His Asp Phe Ile Thr Arg Leu Pro Gln Gly Tyr Asp Thr Glu Val Gly  
 420 425 430  
 Glu Leu Gly Gly Gln Leu Ser Gly Gly Gln Arg Gln Ala Val Ala Ile  
 435 440 445  
 Ala Arg Ala Leu Leu Arg Asp Pro Arg Ile Leu Ile Leu Asp Glu His  
 450 455 460  
 Thr Ser Ala Leu Asp Asn Glu Ser Gln Gln Val Glu Gln Glu Ile  
 465 470 475 480  
 Leu Ala Ala Lys Gly Ser Gly Arg Ala Val Leu Met Val Thr Gly Arg  
 485 490 495  
 Ala Ala Leu Ala Ala Arg Ala Gln Arg Val Val Val Leu Glu Gly Gly  
 500 505 510  
 Glu Val Arg Gln Glu Gly Pro Pro His Glu Val Val Arg Pro Val Ser  
 515 520 525  
 Leu Xaa Ala Gly Leu Gly Thr Thr Arg Glu His Arg Gly Arg Gly Thr  
 530 535 540  
 Glu Gly  
 545

<210> 46  
 <211> 600  
 <212> PRT

<213> Gallus sp.

<400> 46

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20 25 30

Lys Glu Ala Lys Ala Trp Val Pro Leu Arg Arg Leu Leu Ala Leu Ala  
 35 40 45

Trp Pro Glu Trp Pro Phe Leu Gly Cys Ala Phe Leu Phe Leu Ala Leu  
 50 55 60

Ala Ala Leu Gly Glu Thr Ser Leu Pro Tyr Cys Thr Gly Arg Ala Val  
65 70 75 80

Asp Val Leu Arg Gln Gly Asp Gly Leu Ala Ala Phe Thr Ala Ala Val  
 85 90 95

Gly Leu Met Cys Leu Ala Ser Ala Ser Ser Ser Leu Phe Ala Gly Cys  
100 105 110

Arg Gly Gly Leu Arg Phe Val Leu Arg Thr Arg Asp Gln Leu Phe Ser  
 115 120 125

Ser Leu Val Tyr Arg Asp Leu Ala Phe Phe Gln Asn Thr Thr Ala Ala  
130 135 140

Glu Leu Ala Ser Arg Leu Thr Thr Asp Val Thr Leu Ala Ser Asn Val  
145 150 155 160

Leu Ala Leu Asn Ile Asn Val Met Leu Arg Asn Leu Gly Gln Val Leu  
165 170 175

Gly Leu Cys Ala Phe Met Leu Gly Leu Ser Pro Arg Leu Thr Met Leu  
180 185 190

Ala Leu Leu Glu Val Pro Leu Ala Val Thr Ala Arg Lys Val Tyr Asp  
195 200 205

Thr Arg His Gln Met Leu Gln Arg Ala Val Leu Asp Ala Ala Ala Asp  
210 215 220

Thr Gly Ala Ala Val Gln Glu Ser Ile Ser Ser Ile Glu Met Val Arg  
225 230 235 240

Val Phe Asn Gly Glu Glu Glu Glu Glu His Arg Tyr Ser Gln Val Leu  
245 250 255

Asp Arg Thr Leu Arg Leu Arg Asp Gln Arg Asp Thr Glu Arg Ala Ile  
260 265 270

Phe Leu Leu Ile Gln Arg Val Leu Gln Leu Ala Val Gln Ala Leu Val  
275 280 285

Leu Tyr Cys Gly His Gln Gln Leu Arg Glu Gly Thr Leu Thr Ala Gly  
 290 295 300  
 Ser Leu Val Ala Phe Ile Leu Tyr Gln Thr Lys Ala Gly Ser Cys Val  
 305 310 315 320  
 Gln Ala Leu Ala Tyr Ser Tyr Gly Asp Leu Leu Ser Asn Ala Val Ala  
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 Ala Cys Lys Val Phe Asp Tyr Leu Asp Trp Glu Arg Pro Val Gly Ala  
 340 345 350  
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 355 360 365  
 Arg Val Ser Phe Ala Tyr Pro Thr Arg Pro Glu Arg Leu Val Leu Gln  
 370 375 380  
 Asp Val Thr Phe Glu Leu Arg Pro Ser Glu Val Thr Ala Leu Ala Gly  
 385 390 395 400  
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 405 410 415  
 Tyr Glu Pro Gly Ala Gly Glu Val Leu Leu Asp Gly Val Pro Leu Arg  
 420 425 430  
 Asp Tyr Glu His Arg Tyr Leu His Arg Gln Val Ala Leu Val Gly Gln  
 435 440 445  
 Glu Pro Val Leu Phe Ser Gly Ser Ile Arg Asp Asn Ile Ala Tyr Gly  
 450 455 460  
 Met Glu Asp Cys Glu Glu Glu Ile Ile Ala Ala Ala Arg Ala Ala  
 465 470 475 480  
 Gly Ala Leu Gly Phe Ile Ser Ala Leu Glu Gln Gly Phe Gly Thr Asp  
 485 490 495  
 Val Gly Glu Arg Gly Gly Gln Leu Ser Ala Gly Gln Lys Gln Arg Ile  
 500 505 510  
 Ala Ile Ala Arg Ala Leu Val Arg Arg Pro Thr Ile Leu Ile Leu Asp  
 515 520 525  
 Glu Ala Thr Ser Ala Leu Asp Gly Asp Ser Asp Ala Met Leu Gln Gln  
 530 535 540  
 Trp Val Arg Asn Gly Gly Asp Arg Thr Val Leu Phe Ile Thr His Gln  
 545 550 555 560  
 Pro Arg Met Leu Glu Lys Ala Asp Arg Ile Val Val Leu Glu His Gly  
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 580 585 590

40043460-GC402

Pro Tyr Ser Arg Leu Leu Gln His  
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<210> 47  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

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21

<210> 48  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 48  
atccgctcac cgccctgg

18

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 49  
ccagcagtc a ctgcacatat

20

<210> 50  
<211> 19  
<212> DNA  
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<400> 50  
aggtggagtgc cgcaaagtt

19

<210> 51  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 51  
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<210> 52  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 52  
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<210> 53  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 53  
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<210> 54  
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<220>  
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